

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 08:45:46 ; Search time 90 Seconds
(without alignments)

1027.946 Million cell updates/sec

Title: US-09-768-781-3

Perfect score: 2316

Sequence: 1 MDRVVEIPPEPNVPVSSLE.....RTRVENSEPPFTEARQSVV 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rhodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939.5	40.6	446	11 Q9QXY7	Q9QXY7 mus musculus
2	152	6.6	395	4 Q9H6D3	Q9H6D3 homo sapien
3	141.5	6.1	505	4 Q96P28	Q96P28 homo sapien
4	138.5	6.0	362	4 Q8TBA0	Q8TBA0 homo sapien
5	130	5.6	362	11 Q8R118	Q8R118 mus musculus
6	129	5.6	439	5 O17386	O17386 caenorhabdi
7	120.5	5.2	382	17 Q9V2C2	Q9V2C2 pyrococcus
8	119.5	5.2	745	10 Q48539	Q48539 oryza sativ
9	119.5	5.2	943	10 Q942C7	Q942C7 oryza sativ
10	119	5.1	223	4 Q9NUG5	Q9NUG5 homo sapien
11	118.5	5.1	783	10 Q9SAK8	Q9SAK8 arabidopsis
12	113.5	4.9	508	16 Q98QC2	Q98QC2 mycoplasma
13	112.5	4.9	424	8 Q9B8Z8	Q9B8Z8 schistosoma
14	112.5	4.9	785	10 Q9SA37	Q9SA37 arabidopsis
15	111.5	4.8	424	8 Q94UX1	Q94UX1 schistosoma
16	109.5	4.7	424	8 Q94UX2	Q94UX2 schistosoma

17	109.5	4.7	424	8 Q94UX6	Q94UX6 schistosoma
18	109.5	4.7	461	16 Q97E21	Q97E21 clostridium
19	109.5	4.7	472	2 O06039	O06039 lactococcus
20	109.5	4.7	498	8 O47543	O47543 chlamydomon
21	109.5	4.7	1776	5 Q963L7	Q963L7 schistosoma
22	108.5	4.7	424	8 Q94UX8	Q94UX8 schistosoma
23	108	4.7	459	8 O21706	O21706 pygathrix b
24	107	4.6	459	8 O21845	O21845 pygathrix b
25	107	4.6	459	8 O21707	O21707 pygathrix b
26	107	4.6	740	16 Q8ZQN3	Q8ZQN3 salmonella
27	106.5	4.6	341	16 Q9PPX3	Q9PPX3 ureaplasma
28	106	4.6	684	16 Q8XN39	Q8XN39 clostridium
29	105.5	4.6	459	8 O21708	O21708 pygathrix b
30	105.5	4.6	459	8 Q955T9	Q955T9 cheirogaleu
31	105.5	4.6	459	8 Q955T7	Q955T7 cheirogaleu
32	105.5	4.6	511	2 Q9XDK3	Q9XDK3 bacteroides
33	105	4.5	740	16 Q8Z874	Q8Z874 salmonella
34	105	4.5	995	5 Q9N3H7	Q9N3H7 caenorhabdi
35	104.5	4.5	741	16 Q8X7V5	Q8X7V5 escherichia
36	104	4.5	960	5 Q960V0	Q960V0 drosophila
37	103.5	4.5	459	8 Q955T8	Q955T8 cheirogaleu
38	103.5	4.5	469	8 Q9B6C8	Q9B6C8 yarrowia li
39	103.5	4.5	503	17 Q9UZC2	Q9UZC2 pyrococcus
40	103.5	4.5	759	16 Q8RB81	Q8RB81 thermoplaea
41	103.5	4.5	858	16 Q9QXH1	Q9QXH1 streptococc
42	103.5	4.5	2143	10 Q9C8A6	Q9C8A6 arabidopsis
43	102.5	4.4	313	5 Q45426	Q45426 caenorhabdi
44	102.5	4.4	403	2 Q8RJL1	Q8RJL1 vibrio chol
45	102.5	4.4	494	16 Q8XN35	Q8XN35 clostridium

ALIGNMENTS

RESULT 1
Q9QXY7 PRELIMINARY; PRT; 446 AA.
AC Q9QXY7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE KX antigen (1810038K19RIK protein).
GN KX OR XK OR 1810038K19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=SKELETAL MUSCLE;
RX MEDLINE=20009522; PubMed=10541802;
RA Collec E., Colin Y., Carbonnet F.; Hattab C., Bertrand O.,
RA Carton J.P., Kim C.L.;
RT "Structure and expression of the mouse homologue of the XK gene";
RL Immunogenetics 50:16-21(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=SKELETAL MUSCLE;
RA Le Van Kim C., Collec E., Colin Y.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guinoteich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AF155511; AAF14527.1; -
DR EMBL; AK007734; BAB2522.1; -
DR MGD; MGI:103569; Xkh.
SQ SEQUENCE 446 AA; 51114 MW; D785FB7B9E28B98B CRC64;

Query Match 40.6%; Score 939.5; DB 11; Length 446;
Best Local Similarity 43.8%; Pred. No. 4.7e-70;
Matches 180; Conservative 85; Mismatches 135; Indels 11; Gaps 4;
QY 33 PPSGILSTLYCGEASALYVRIYKNSERYTYTTFSPFESSIMVQLTFVHRDL 92
DB 3 PPSVIAVSLFVFAETAALYLSSTYSAGDRMMQVLTLLPSLPCALVQPTLLFVHRDL 62
QY 93 AKOKPLSLFHLIILGVPVIRCLEAMIKYTLTWKKEOEPEYVSLTRKK-MLIDGSEVLIE 151
DB 63 SRDPLALLMHLQLGPLYRCCEVFCYC---QSDNEEPVSVIKKQMPKDGUSEBE 119
QY 152 WEVGHISIRTLAMHRNAYKRMQSOIAPLGSVPQLTLYQLVSLISAEVPLGRVVLVMSVLS 211
DB 120 KEVGOAEKLIHRSAPSASVIAQFLGSAPQLTLQVLTIVLEQNIITGRCFIMTSLLS 179
QY 212 VTYGATLCNMLAIQIKYDDYKIRGLPGLVLCITWRTLEITSRLIILVPLSATLKLKAVP 271
DB 180 IVYGALRCNLAIKIKYDEYEVKVKPLAYCFLRSFEIATRVIVLFTSVLKIIWVA 239
QY 272 FLVNLFIILPEPWIKFWRGSAQPNNEKNFNRVGTGLVLSIVTLYAGNFCWSALQ 331
DB 240 VILVNFSPPLYPVIFVWCSSGSPENIEKALSRTGTVIVLCFTLLVAGINMFCWSAVQ 299
QY 332 LRLADRLVDKQNGHMGHLYSVRLVENVIMLVKFPFGVKVLYNCHSLIALQLIITAY 391
DB 300 LKIDNPELISQSNWYRLIYYMTRFIENSVLILLWYFFKTDIYVYVYCAPLILQLLIGY 359
QY 392 LISIDFMLFPQYLHPLSLTHNVVD---YLHCVCCHQHPRTVENSEP 438
DB 360 CTGILFVLVYQFHPCKGLFSSVSSEFRALLRCACWSS---LARKSSEP 407

RESULT 2
Q9H6D3 ID Q9H6D3 PRELIMINARY; PRT; 395 AA.
AC Q9H6D3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CNA: FLJ22371 fis, Clone HRC06680 (Hypothetical 44.7 kDa protein)
DE (Similar to hypothetical protein FLJ10307).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Strausberg R.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026024; BAB15326.1; -
DR EMBL; BC013379; AAHL3379.1; -
DR EMBL; BC028564; AAH28564.1; -
SQ SEQUENCE 395 AA; 44654 MW; 23199BAEEA6964C6 CRC64;
Query Match 6.8%; Score 152; DB 4; Length 395;
Best Local Similarity 21.1%; Pred. No. 0.00012;
Matches 82; Conservative 71; Mismatches 136; Indels 100; Gaps 17;
QY 75 MFSSIMVQLTIFVHRDLAKDKPLSLFMHLIILGVPVIRCLEAMIKYTLTWKKEOEPEYV 134
DB 62 LFSWLWLRADPAGLHGSQPPRRCLAL-LHLQLGLYLYRCVQLRQGLLVW---QQEEP-- 115
QY 135 SLTRKMLIDGEEVLIEWEVGHISIRTLAMHRNAYKRMQSOIAPLGSVPQLTLYQLVSLIS 194
DB 116 -----SEFDLAYA-DFLALD---ISMRLRFETLETAPQLTLVLAIMLOS 156
QY 195 AEVPLGRVVLVMSVLSVYTGATLCNMLAIQIKYDDY-----KIRLGPLEVLCIT 244
DB 157 GRAEYQVQWIGCTSFGLISWALL-----DYHRAURTCLPSKPLLGSGSVIYF 204
QY 245 IWRTEITSRLLIILVLSATL-KLKAVPFLVNLFIILFEPWIKFWRGSAQ-MPNNEKN 302
DB 205 LWNLLLPVRLVAVLPSYVALHFLGLMLVLL---WV--WLQGTDFMPDPSSW 259
QY 303 PSRVGTLLVLSIVTLYAGNFCWSALQRLADRLVDKQNGHMGHLYSVRLVENV 362
DB 260 LYRVTV-----ATILY-----FSWFN-----VAEGTRGRAIHFALSLSDSIL 298
QY 363 MVLVFKFPGVKVLYNCHSLIALQLII-----AYLISIDFMLFPQYLHPLSLTHNVV 417
DB 299 LVATVTHS-----SWLPSGIPQLQWLPVGCPCFLGLALRLVYTHWLHP----- 343
QY 418 DYLCVCCHQHPRTVENSEPFFETEARQ 446
DB 344 ----SCCWKPDQPDQVGARSLLSPGYQ 367

RESULT 3
Q96PZ8 ID Q96PZ8 PRELIMINARY; PRT; 505 AA.
AC Q96PZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIAA1889 protein (Fragment).
GN KIAA1889.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins".
RL DNA Res. 8:179-187(2001).
DR EMBL; AB067476; BAB67782.1; -
FT NON TER 1
SQ SEQUENCE 505 AA; 56911 MW; D764B96BC29B3623 CRC64;
Query Match 6.1%; Score 141.5; DB 4; Length 505;
Best Local Similarity 20.6%; Pred. No. 0.0011;

[illegible]

DR Pfam; PF00361; oxidored q1; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 424 AA; 47741 MW; 377C53E61F57D72 CRC64;

Query Match 4.9%; Score 112.5; DB 8; Length 424;
Best Local Similarity 19.5%; Pred. No. 0.24;
Matches 90; Conservative 77; Mismatches 156; Indels 139; Gaps 20;

QY 32 TPFFSILSTFLYCGEASALYVRIYKNSETYRTYTFSEFMSSIMVOLT-LIFVHR 90
DB 18 TPFLILFYSSIVWSDSSVMVGKYLCDGLVIIDT-----LSCLMIFLTSIIWLV 70
QY 91 DIADKPLSLFMHLILGVPVIRCLAMIKY-----LTLWKKEQEPEYVSLTRKQMLD 145
DB 71 WLVGSKDIVLP-----ISVFSAMITYVVSNSLVFWFFYELS-----IISALYWLIVG 117
QY 146 ----REVLIENVEGHSIRTLAMHRNAYKMSQIAPLGSVPOLTVQLXVLSIAEVLGR 201
DB 118 SPYPERYISSMYFGYI-----LLSSVPALLGICITGLNSGSF---N 156
QY 202 VLVMFVSLVSVTYGATLCNML-----AIOIKVDDYKIRLGP 237
DB 157 VILMDKGMDCSYGAFLIIMFLTKIPVPPHGWLPVHAESPVSIILSGYIMKGL 216
QY 238 LEVLCTITWRTLEITSRLLILVLFSATLKLKAVPLVLNLFILPEPWIKWRSGAOMPN 297
DB 217 VGLVRLCGMLLID-----YIYFSTFLCYVVYLV-----NAVFECDKRWLAYLSLH 266
QY 298 NIEKNFSRVGTLWL-----ISVTIYAGINFSCWALQRLADRL 339
DB 267 IL-----IGVCILLSTYCGDYLAFLYCLGHLSVALLFWI-----WFGYE----- 308
QY 340 VDKGNQCHMGHLGHSYVRLVENVIMVLP-----KPGF-VKVLNY---CHSLIALQ 386
DB 309 ISGRNMGWILVKIFGGGIMHFMFGFVLNVCGPPALQFGELWLVINYITLGDIIILL 368
QY 387 LIAYLIS---IDFMFLPFQVLPULRSIFTN--VDVLHCV 423
DB 369 LVSIIYFSGSIIGFIYGLVICSPINTSYEGGLDNFLFCI 410

RESULT 14
Q9SA37
ID Q9SA37 PRELIMINARY; PRT; 785 AA.
AC Q9SA37
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F309.18 protein.
GN F309.18
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaya V.S., Schwartz J., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J., Li J., Kremenetskaia I., Liu A., Luros J., Gonzalez A.,
RA Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federespiel N.A., Theologis A.;
RL "The sequence of BAC F309 from Arabidopsis thaliana chromosome 1.";
RN Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC006341; AAC34690.1; -
DR InterPro; IPR000676; NaH Exchng.

DR Pfam; PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 785 AA; 88908 MW; 3830426AAA6CB1 CRC64;

Query Match 4.9%; Score 112.5; DB 10; Length 785;
Best Local Similarity 19.7%; Pred.No.0.45;
Matches 89; Conservative 84; Mismatches 172; Indels 107; Gaps

Qy	37 ILFSFLY-----CGEAAAS-----ALYMVRIYRKNSETMYTYSFFMFSSIMVOL 83 :: :: :: :: :: :: :: :: :: :: :: :
Dd	30 LVSPFPFVLKFCGAGPVAQLAGIVLSLTIIRKVHEFFLQKDSASYIFFSFLRT 89 :: :: :: :: :: :: :: :: :: :: :: :
Qy	84 TLIP-VHRDLAKPKSLFMHLLILGPVRICLEAMIKYTLMKKEEQBEPYVSLTRKKWL 142 :: :: :: :: :: :: :: :: :: :: :: :
Dd	90 AFVELIGLEDLD----FMKRNLKNSIITLGSLVISGIIMW-----PFELFIREFMQ 138 :: :: :: :: :: :: :: :: :: :: :: :
Qy	143 IDGS-----EVILEWEVGHS-IRTLAMHRNAYKRNISOIAFLGS 180 :: :: :: :: :: :: :: :: :: :: :: :
Dd	139 IKGDPLTFYLAFILITSNTAAPVVRSIIIDMKLTSEIGRLAISCSGLFTIEITI-- 192 :: :: :: :: :: :: :: :: :: :: :: :
Qy	181 VPQTYOLYVSLISAEBVLGRVVMVFSLSVSYTGATLCNMLAIQKYDDYKIRLGPLE- 239 :: :: :: :: :: :: :: :: :: :: :: :
Dd	193 ---FIYTVLVSPISGTWTADIFIYPSPATGVIIILTNRFLASMLPRKPKEKYLKAETLAF 249 :: :: :: :: :: :: :: :: :: :: :: :
Qy	240 -VLCITIWRTL---ITSRLILIY---LFSAULK-----LKAVPLVINFLLIPEPIWK 287 :: :: :: :: :: :: :: :: :: :: :: :
Dd	250 IILILIALTIESNNSTLPFIIIGLMPREGTKYRTLIQRLSYPHFVLVPYFGVIG 309 :: :: :: :: :: :: :: :: :: :: :: :
Qy	288 FWRSGAQMNINIKESRYGTLVVLISVTLYAGINFSC-----WSALOURLADR 338 :: :: :: :: :: :: :: :: :: :: :: :
Dd	310 FRFS-----VNSLTRHYLVGMTVALSLGKLGLVLPACSFUKIPQKWFLFWLSTMVSK- 364 :: :: :: :: :: :: :: :: :: :: :: :
Qy	339 LVDKGQNGHMGLHYSRVLNVVIMVLPKFQGKVLNLYCHSLIALOLIITYLTS-ID 396 :: :: :: :: :: :: :: :: :: :: :: :
Dd	365 -----GHIGL---VLSDSN---LMYKRWTPPV-----HDMEFAALVMTLLSGVIT 405 :: :: :: :: :: :: :: :: :: :: :: :
Qy	397 FMILLFQQ---YHLPLSLPTHNVVYLHCVC 425 :: :: :: :: :: :: :: :: :: :: :: :
Dd	406 SLLLRSOXSFAHIKTSELFDTTBELRVLC 437 :: :: :: :: :: :: :: :: :: :: :: :

RESULT 15

Q94UX1	ID Q94UX1 PRELIMINARY; PRT; 424 AA.
AC	O94DX1;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	NADH dehydrogenase subunit 4.
GN	NAD4.
OS	Schistosoma japonicum (Blood fluke).
OG	Mitochondrion
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OX	Schistosomatoidae; Schistosomatiidae; Schistosoma.
NCBI_TaxId=6182;	
RN	[1]
RX	SEQUENCE FROM N.A.
RA	MEDLINE=20349913; PubMed=10889225;
RA	Le T.H., Blair D.; Agatesuma T., Humair P.F., Campbell N.J., Iwagami M., Littlewood D.T., Peacock B., Johnston D.A., Bartley J., Rollinson D., Herniou E.A., Zarlinga D.S., McManus D.P.;
RA	"Phylogenies inferred from mitochondrial gene orders-a cautionary tale from the parasitic flatworms.";
RM	Mol. Biol. Evol. 17:1123-1125(2000). [2]
RN	[2]
RP	SEQUENCE FROM N.A.
RR	Le T.H., Blair D., McManus D.P.;
RT	"Revisiting limited genetic variation within Schistosoma japonicum populations."
RT	Submitted (AUG-2001) to the ENBL/GenBank/DBJ databases.
CC	-1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+)+ UBIQUINOL.
ENBL; AP412213; AALI2155.1; -	
InterPro; IPRO01750; Oxidored g1.	
DR . Pfam; PP00361; oxidored gl; 1.	

